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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Jun 08 20:42:44 EDT 2007

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Application No: 10713978 Version No: 3.1

Input Set:**Output Set:**

Started: 2007-06-08 20:42:29.200
Finished: 2007-06-08 20:42:36.516
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 316 ms
Total Warnings: 76
Total Errors: 53
No. of SeqIDs Defined: 129
Actual SeqID Count: 129

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
E 257	Invalid sequence data feature in <221> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
E 257	Invalid sequence data feature in <221> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
E 257	Invalid sequence data feature in <221> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
E 257	Invalid sequence data feature in <221> in SEQ ID (30)
E 257	Invalid sequence data feature in <221> in SEQ ID (30)

Input Set:

Output Set:

Started: 2007-06-08 20:42:29.200
Finished: 2007-06-08 20:42:36.516
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 316 ms
Total Warnings: 76
Total Errors: 53
No. of SeqIDs Defined: 129
Actual SeqID Count: 129

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
E 257	Invalid sequence data feature in <221> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
E 257	Invalid sequence data feature in <221> in SEQ ID (32)
E 257	Invalid sequence data feature in <221> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
E 257	Invalid sequence data feature in <221> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
E 257	Invalid sequence data feature in <221> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (46)
E 257	Invalid sequence data feature in <221> in SEQ ID (47)
E 257	Invalid sequence data feature in <221> in SEQ ID (48)
E 257	Invalid sequence data feature in <221> in SEQ ID (49)
E 257	Invalid sequence data feature in <221> in SEQ ID (50) This error has occurred more than 20 times, will not be displayed
W 251	Found intentionally skipped sequence in SEQID (63)

Input Set:

Output Set:

Started: 2007-06-08 20:42:29.200
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Total Warnings: 76
Total Errors: 53
No. of SeqIDs Defined: 129
Actual SeqID Count: 129

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (64)

SEQUENCE LISTING

<110> Yaffe, Michael B.
 Elia, Andrew E.H.
 Rellos, Peter
 Cantley, Lewis C.
 Smerdon, Stephen J.
 Manke, Isaac

<120> Computer Comprising Atomic Coordinates of a PLK-1 Polo-Box Domain
 and Uses Thereof

<130> 01997/545003

<140> US 10/713,978
 <141> 2003-11-14

<150> US 60/487,899
 <151> 2003-07-17

<150> US 60/485,641
 <151> 2003-07-08

<150> US 60/426,132
 <151> 2002-11-14

<160> 129

<170> PatentIn version 3.3

<210> 1
 <211> 603
 <212> PRT
 <213> Homo sapien

<400> 1

Met Ser Ala Ala Val Thr Ala Gly Lys Leu Ala Arg Ala Pro Ala Asp
 1 5 10 15

Pro Gly Lys Ala Gly Val Pro Gly Val Ala Ala Pro Gly Ala Pro Ala
 20 25 30

Ala Ala Pro Pro Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
 35 40 45

Ser Arg Arg Arg Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
 50 55 60

Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala
 65 70 75 80

Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Arg Glu
85 90 95

Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His
100 105 110

Val Val Gly Phe His Gly Phe Phe Glu Asp Asn Asp Phe Val Phe Val
115 120 125

Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Leu His Lys Arg
130 135 140

Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile
145 150 155 160

Val Leu Gly Cys Gln Tyr Leu His Arg Asn Arg Val Ile His Arg Asp
165 170 175

Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile
180 185 190

Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys
195 200 205

Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Ser
210 215 220

Lys Lys Gly His Ser Phe Glu Val Asp Val Trp Ser Ile Gly Cys Ile
225 230 235 240

Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu Thr Ser Cys Leu
245 250 255

Lys Glu Thr Tyr Leu Arg Ile Lys Lys Asn Glu Tyr Ser Ile Pro Lys
260 265 270

His Ile Asn Pro Val Ala Ala Ser Leu Ile Gln Lys Met Leu Gln Thr
275 280 285

Asp Pro Thr Ala Arg Pro Thr Ile Asn Glu Leu Leu Asn Asp Glu Phe
290 300

Phe Thr Ser Gly Tyr Ile Pro Ala Arg Leu Pro Ile Thr Cys Leu Thr

305		310		315		320									
Ile	Pro	Pro	Arg	Phe	Ser	Ile	Ala	Pro	Ser	Ser	Leu	Asp	Pro	Ser	Asn
				325						330				335	
Arg	Lys	Pro	Leu	Thr	Val	Leu	Asn	Lys	Gly	Leu	Glu	Asn	Pro	Leu	Pro
			340						345				350		
Glu	Arg	Pro	Arg	Glu	Lys	Glu	Glu	Pro	Val	Val	Arg	Glu	Thr	Gly	Glu
		355						360					365		
Val	Val	Asp	Cys	His	Leu	Ser	Asp	Met	Leu	Gln	Gln	Leu	His	Ser	Val
		370					375					380			
Asn	Ala	Ser	Lys	Pro	Ser	Glu	Arg	Gly	Leu	Val	Arg	Gln	Glu	Glu	Ala
385						390					395				400
Glu	Asp	Pro	Ala	Cys	Ile	Pro	Ile	Phe	Trp	Val	Ser	Lys	Trp	Val	Asp
				405					410					415	
Tyr	Ser	Asp	Lys	Tyr	Gly	Leu	Gly	Tyr	Gln	Leu	Cys	Asp	Asn	Ser	Val
			420						425					430	
Gly	Val	Leu	Phe	Asn	Asp	Ser	Thr	Arg	Leu	Ile	Leu	Tyr	Asn	Asp	Gly
		435						440					445		
Asp	Ser	Leu	Gln	Tyr	Ile	Glu	Arg	Asp	Gly	Thr	Glu	Ser	Tyr	Leu	Thr
		450					455				460				
Val	Ser	Ser	His	Pro	Asn	Ser	Leu	Met	Lys	Lys	Ile	Thr	Leu	Leu	Lys
465						470				475					480
Tyr	Phe	Arg	Asn	Tyr	Met	Ser	Glu	His	Leu	Leu	Lys	Ala	Gly	Ala	Asn
				485					490					495	
Ile	Thr	Pro	Arg	Glu	Gly	Asp	Glu	Leu	Ala	Arg	Leu	Pro	Tyr	Leu	Arg
			500						505					510	
Thr	Trp	Phe	Arg	Thr	Arg	Ser	Ala	Ile	Ile	Leu	His	Leu	Ser	Asn	Gly
		515					520					525			
Ser	Val	Gln	Ile	Asn	Phe	Phe	Gln	Asp	His	Thr	Lys	Leu	Ile	Leu	Cys
530						535					540				

Pro Leu Met Ala Ala Val Thr Tyr Ile Asp Glu Lys Arg Asp Phe Arg
545 550 555 560

Thr Tyr Arg Leu Ser Leu Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu
565 570 575

Ala Ser Arg Leu Arg Tyr Ala Arg Thr Met Val Asp Lys Leu Leu Ser
580 585 590

Ser Arg Ser Ala Ser Asn Arg Leu Lys Ala Ser
595 600

<210> 2
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = Pro or Phe

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Pro or a hydrophobic amino acid

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = Ala, Gln, or a hydrophobic amino acid

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = Thr, Gln, His or Met

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = phosphorylated Thr or phosphorylated Ser

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Pro or any amino acid

<400> 2

Xaa Xaa Xaa Xaa Ser Xaa Xaa
1 5

<210> 3

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MOD_RES

<222> (8)..(8)

<223> PHOSPHORYLATION

<400> 3

Met Ala Gly Pro Met Gln Ser Thr Pro Leu Asn Gly Ala Lys Lys
1 5 10 15

<210> 4

<211> 685

<212> PRT

<213> Homo sapiens

<400> 4

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
1 5 10 15

Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
20 25 30

Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
145 150 155 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
165 170 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
180 185 190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
195 200 205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
210 215 220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
225 230 235 240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
245 250 255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
260 265 270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
275 280 285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
290 295 300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
305 310 315 320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln

325	330	335
Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro		
340	345	350
Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala		
355	360	365
Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr		
370	375	380
His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His		
385	390	395
Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr		
405	410	415
Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr		
420	425	430
Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile		
435	440	445
Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu		
450	455	460
Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg		
465	470	475
Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln		
485	490	495
Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn		
500	505	510
Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu		
515	520	525
Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val		
530	535	540
His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp		
545	550	555
		560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
610 615 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625 630 635 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
645 650 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
660 665 670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
675 680 685

<210> 5
<211> 646
<212> PRT
<213> Homo sapiens

<400> 5

Met Glu Pro Ala Ala Gly Phe Leu Ser Pro Arg Pro Phe Gln Arg Ala
1 5 10 15

Ala Ala Ala Pro Ala Pro Pro Ala Gly Pro Gly Pro Pro Pro Ser Ala
20 25 30

Leu Arg Gly Pro Glu Leu Glu Met Leu Ala Gly Leu Pro Thr Ser Asp
35 40 45

Pro Gly Arg Leu Ile Thr Asp Pro Arg Ser Gly Arg Thr Tyr Leu Lys
50 55 60

Gly Arg Leu Leu Gly Lys Gly Gly Phe Ala Arg Cys Tyr Glu Ala Thr
65 70 75 80

Asp Thr Glu Thr Gly Ser Ala Tyr Ala Val Lys Val Ile Pro Gln Ser
85 90 95

Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Leu Asn Glu Ile Glu
100 105 110

Leu His Arg Asp Leu Gln His Arg His Ile Val Arg Phe Ser His His
115 120 125

Phe Glu Asp Ala Asp Asn Ile Tyr Ile Phe Leu Glu Leu Cys Ser Arg
130 135 140

Lys Ser Leu Ala His Ile Trp Lys Ala Arg His Thr Leu Leu Glu Pro
145 150 155 160

Glu Val Arg Tyr Tyr Leu Arg Gln Ile Leu Ser Gly Leu Lys Tyr Leu
165 170 175

His Gln Arg Gly Ile Leu His Arg Asp Leu Lys Leu Gly Asn Phe Phe
180 185 190

Ile Thr Glu Asn Met Glu Leu Lys Val Gly Asp Phe Gly Leu Ala Ala
195 200 205

Arg Leu Glu Pro Pro Glu Gln Arg Lys Lys Thr Ile Cys Gly Thr Pro
210 215 220

Asn Tyr Val Ala Pro Glu Val Leu Leu Arg Gln Gly His Gly Pro Glu
225 230 235 240

Ala Asp Val Trp Ser Leu Gly Cys Val Met Tyr Thr Leu Leu Cys Gly
245 250 255

Ser Pro Pro Phe Glu Thr Ala Asp Leu Lys Glu Thr Tyr Arg Cys Ile
260 265 270

Lys Gln Val His Tyr Thr Leu Pro Ala Ser Leu Ser Leu Pro Ala Arg
275 280 285

Gln Leu Leu Ala Ala Ile Leu Arg Ala Ser Pro Arg Asp Arg Pro Ser

290

295

300

Ile Asp Gln Ile Leu Arg His Asp Phe Phe Thr Lys Gly Tyr Thr Pro
305 310 315 320

Asp Arg Leu Pro Ile Ser Ser Cys Val Thr Val Pro Asp Leu Thr Pro
325 330 335

Pro Asn Pro Ala Arg Ser Leu Phe Ala Lys Val Thr Lys Ser Leu Phe
340 345 350

Gly Arg Lys Lys Lys Ser Lys Asn His Ala Gln Glu Arg Asp Glu Val
355 360 365

Ser Gly Leu Val Ser Gly Leu Met Arg Thr Ser Val Gly His Gln Asp
370 375 380

Ala Arg Pro Glu Ala Pro Ala Ala Ser Gly Pro Ala Pro Val Ser Leu
385 390 395 400

Val Glu Thr Ala Pro Glu Asp Ser Ser Pro Arg Gly Thr Leu Ala Ser
405 410 415

Ser Gly Asp Gly Phe Glu Glu Gly Leu Thr Val Ala Thr Val Val Glu
420 425 430

Ser Ala Leu Cys Ala Leu Arg Asn Cys Ile Ala Phe Met Pro Pro Ala
435 440 445

Glu Gln Asn Pro Ala Pro Leu Ala Gln Pro Glu Pro Leu Val Trp Val
450 455 460

Ser Lys Trp Val Asp Tyr Ser Asn Lys Phe Gly Phe Gly Tyr Gln Leu
465 470 475 480

Ser Ser Arg Arg Val Ala Val Leu Phe Asn Asp Gly Thr His Met Ala
485 490 495

Leu Ser Ala Asn Arg Lys Thr Val His Tyr Asn Pro Thr Ser Thr Lys
500 505 510

His Phe Ser Phe Ser Val Gly Ala Val Pro Arg Ala Leu Gln Pro Gln
515 520 525

Leu Gly Ile Leu Arg Tyr Phe Ala Ser Tyr Met Glu Gln His Leu Met
530 535 540

Lys Gly Gly Asp Leu Pro Ser Val Glu Glu Val Glu Val Pro Ala Pro
545 550 555 560

Pro Leu Leu Leu Gln Trp Val Lys Thr Asp Gln Ala Leu Leu Met Leu
565 570 575

Phe Ser Asp Gly Thr Val Gln Val Asn Phe Tyr Gly Asp His Thr Lys
580 585 590

Leu Ile Leu Ser Gly Trp Glu Pro Leu Leu Val Thr Phe Val Ala Arg
595 600 605

Asn Arg Ser Ala Cys Thr Tyr Leu Ala Ser His Leu Arg Gln Leu Gly
610